

OM protein - protein search, using sw model

Run on: November 16, 2006, 22:47:18 ; Search time 156 Seconds
(without alignments)
35.578 Million cell updates/sec

Title: FRSSRQ

Perfect score: 29

Sequence: 1 frssrq 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	99	2 Q5NM07_ZYMMO	Q5nm07 zymomonas m
2	29	100.0	296	2 Q8ZT49_PYRAE	Q8zt49 pyrobaculum
3	29	100.0	487	2 Q5L502_CHLAB	Q5l502 chlamydothi
4	29	100.0	497	1 PBN3_ADE12	P36716 human adeno
5	29	100.0	555	2 Q2KRX5_ADE16	Q2kxr5 human adeno
6	29	100.0	621	2 Q9UUG2_SCHPO	Q9uug2 schizosacch
7	29	100.0	629	2 Q4FED3_CHLAB	Q4fed3 chlamydothi
8	29	100.0	648	2 Q4VA42_MOUSE	Q4va42 mus musculu
9	29	100.0	648	2 Q8BHK4_MOUSE	Q8bhnk4 m 13 days e
10	29	100.0	649	2 Q6P7P7_RAT	Q6p7p7 rattus norv
11	29	100.0	708	2 Q9LJG1_ARATH	Q9ljg1 arabidopsis
12	29	100.0	1033	1 YD56_SCHPO	Q10309 schizosacch
13	29	100.0	1172	2 Q5CLH4_CHYHO	Q5clh4 cryptospori
14	29	100.0	1173	2 Q5CV20_CRYPV	Q5cv20 cryptospori
15	29	100.0	1889	2 Q41IK4_GIBZE	Q41ik4 gibberella

16	29	100.0	3380	1 APLP_LOCMI	Q9u943 locusta mig
17	26	89.7	85	2 Q1G7F6_9DELT	Q3g7f6 pelobacter
18	26	89.7	108	2 Q2LY38_9DELT	Q2ly38 syntrophus
19	26	89.7	111	2 Q9FTX6_ORISA	Q9ftx6 oryza sativ
20	26	89.7	115	2 Q8SXZ9_DROME	Q8sxz9 drosophila
21	26	89.7	128	2 Q9HAF0_HUMAN	Q9haf0 homo sapien
22	26	89.7	130	2 Q3XMP8_9PROT	Q3xmp8 magnetococc
23	26	89.7	143	2 Q9Z6J0_CHLPN	Q9z6j0 chlamydia p
24	26	89.7	156	2 Q3GUE0_MARHY	Q3gue0 marinobacte
25	26	89.7	179	1 RM49_DROME	Q9vv13 drosophila
26	26	89.7	180	2 Q6YNM8_9LACO	Q6ynm8 lactobacill
27	26	89.7	184	2 Q8CYM5_OCEIH	Q8cym5 oceanobacil
28	26	89.7	200	2 Q2SCZ4_9GAMM	Q2scz4 hahella che
29	26	89.7	213	2 Q36WY0_RHOPA	Q36wy0 rhodopsendo
30	26	89.7	231	2 Q372V7_RHOPA	Q372v7 rhodopsendo
31	26	89.7	236	2 Q89TW8_BRAJA	Q89tw8 bradyrhizob
32	26	89.7	237	2 Q3TU24_MOUSE	Q3tu24 mus musculu
33	26	89.7	238	2 Q3KRE1_RAT	Q3kre1 rattus norv
34	26	89.7	244	1 CF141_HUMAN	Q5szdl homo sapien
35	26	89.7	246	2 Q2SSH0_9SPHI	Q2ssh0 salinibacte
36	26	89.7	248	1 TRPC_SULSO	Q06121 sulfolobus
37	26	89.7	253	2 Q8RLF9_BRAJA	Q8rlf9 bradyrhizob
38	26	89.7	259	2 Q8A8U1_BACTN	Q8a8u1 bacteroides
39	26	89.7	262	2 Q6OVSE_CABBR	Q6ovs6 caenorhabdi
40	26	89.7	266	2 Q3M741_ANAVT	Q3m741 anabaena va
41	26	89.7	266	2 Q8YQV3_ANASP	Q8yqv3 anabaena sp
42	26	89.7	274	2 Q5AQE7_EMENI	Q5aqe7 aspergillus
43	26	89.7	283	2 Q9V176_TRIVA	Q9v176 trichomonas
44	26	89.7	286	2 Q3F3C3_9BURK	Q3fc3 burkholderi
45	26	89.7	291	1 POPD3_MOUSE	Q9ea81 mus musculu

ALIGNMENTS

RESULT 1

Q5NM07_ZYMMO

ID Q5NM07_ZYMMO PRELIMINARY; PRT; 99 AA.

AC Q5NM07_ZYMMO PRELIMINARY; PRT; 99 AA.

DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.

DT 01-FEB-2005, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Hypothetical protein.

GN OrderedLocNames=ZM01629;

OS Zymomonas mobilis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;

OC Sphingomonadaceae; Zymomonas.

OX NCBI_TaxID=542;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=ATCC 31821 / ZM4 / CP4;

RX PubMed=15592456; DOI=10.1038/nbt1045;

RA Seo J.-S., Chong H., Park H.-S., Yoon K.-O., Jung C., Kim J.-J.,

RA Hong J.-H., Kim H., Kim J.-H., Kil J.-I., Park C.-J., Oh H.-M.,

RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.-Y.,

RA Kang H.-L., Lee S.-Y., Lee K.-J., Kang H.-S.;

RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis

OM protein - protein search, using sw model

Run on: November 16, 2006, 22:52:33 ; Search time 20.4 Seconds
(without alignments)
28.299 Million cell updates/sec

Title: FRSSRQ
Perfect score: 29
Sequence: 1 frssrq 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	497	1 S33938	penton protein (II
2	29	100.0	621	2 T39204	hypothetical prote
3	29	100.0	1033	2 T39030	probable calcium-t
4	26	89.7	143	2 B86624	HTH transcription
5	26	89.7	143	2 G72000	Hch transcription
6	26	89.7	248	1 S50179	indole-3-glycerol-
7	26	89.7	248	2 C40835	indole-3-glycerol-
8	26	89.7	266	2 AB2270	hypothetical prote
9	26	89.7	380	2 I38435	angiotensin recept
10	26	89.7	544	1 S41389	penton protein (II
11	26	89.7	571	1 XZADH5	penton protein (II
12	26	89.7	589	2 AG2932	GDEF family prote
13	26	89.7	589	2 H98349	phototransducer, m

14	26	89.7	638	2 D85435	BEL1-like homeobox
15	26	89.7	776	2 C83411	secretion protein
16	26	89.7	822	2 S26872	DNA-directed RNA p
17	26	89.7	917	2 S26365	surface-layer prot
18	26	89.7	991	2 S43891	dna exoribonucleas
19	26	89.7	3623	2 T08618	intrinsic factor-B
20	25	86.2	221	2 S70755	hypothetical prote
21	25	86.2	221	2 T06815	probable embryonic
22	25	86.2	222	2 A75416	conserved hypoteth
23	25	86.2	241	2 AC3000	hypothetical prote
24	25	86.2	278	2 S09662	hypothetical prote
25	25	86.2	286	2 T23066	hypothetical prote
26	25	86.2	380	2 AI2185	hypothetical prote
27	25	86.2	399	2 T21586	hypothetical prote
28	25	86.2	404	2 H82125	hypothetical prote
29	25	86.2	419	2 D69202	5-enolpyruvylshiki
30	25	86.2	427	2 T41257	hypothetical prote
31	25	86.2	546	2 AF2268	type II site-speci
32	25	86.2	658	2 C81860	DNA mismatch repai
33	25	86.2	663	2 T24881	hypothetical prote
34	25	86.2	718	2 T20673	hypothetical prote
35	25	86.2	749	2 E87599	hypothetical prote
36	25	86.2	817	2 A47716	dolichyl-phosphate
37	25	86.2	1614	2 T29861	hypothetical prote
38	25	86.2	2025	2 T03884	hypothetical prote
39	25	86.2	4116	2 T13719	calo protein - fru
40	24	82.8	33	2 H43284	zinc finger protei
41	24	82.8	37	2 A23617	conglutin delta-2
42	24	82.8	49	2 T02026	glycine-rich prote
43	24	82.8	118	2 S55185	hypothetical prote
44	24	82.8	136	2 T49582	hypothetical prote
45	24	82.8	139	2 T13131	protein gp45 - pha

ALIGNMENTS

RESULT 1

S33938
penton protein (III) - human adenovirus 12
C:Species: Mastadenovirus h12 (human adenovirus 12)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S33938
R:Sprenkel, J.
submitted to the EMBL Data Library, June 1993
A:Reference number: S33928
A:Accession: S33938
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <SPR>
A:Cross-references: UNIPROT:P36716; UNIPARC:UPI0000011159C; EMBL:X73487;
NID:g313361; PIDN:CAA51887.1; PID:g313372
C:Superfamily: adenovirus penton protein

Query Match 100.0%; Score 29; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OM protein - protein search, using sw model

Run on: November 16, 2006, 22:46:28 ; Search time 117.6 Seconds
(without alignments)
23.127 Million cell updates/sec

Title: FRSSRQ
Perfect score: 29
Sequence: 1 frssrq 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_8.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001s.*
 - 5: Geneseq2002s.*
 - 6: Geneseq2003as.*
 - 7: Geneseq2003bs.*
 - 8: Geneseq2004s.*
 - 9: Geneseq2005s.*
 - 10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	8	ADU05742
2	29	100.0	6	9	ADZ79589
3	29	100.0	6	9	AE897528
4	29	100.0	6	9	AEC32751
5	29	100.0	168	8	ADY05168
6	29	100.0	984	7	ABM88980
7	29	100.0	1080	8	ADN19557

8	26	89.7	6	10	ASEG01602
9	26	89.7	7	10	ASEG01603
10	26	89.7	8	10	ASEG01604
11	26	89.7	43	9	AED82191
12	26	89.7	60	4	AAU40603
13	26	89.7	60	6	ABM37122
14	26	89.7	62	4	ABG14576
15	26	89.7	106	7	ABM89190
16	26	89.7	108	4	AAO02468
17	26	89.7	127	4	AAO09629
18	26	89.7	128	4	AA893808
19	26	89.7	129	4	AAO10632
20	26	89.7	143	2	AAO10632
21	26	89.7	143	6	ABU26978
22	26	89.7	148	7	ABO81572
23	26	89.7	159	8	ADK72192
24	26	89.7	176	4	ABG14574
25	26	89.7	179	4	ABB59235
26	26	89.7	179	4	ABG14570
27	26	89.7	195	3	AAG44053
28	26	89.7	220	4	AAO13791
29	26	89.7	226	4	ABB17770
30	26	89.7	234	8	ADY10983
31	26	89.7	244	6	ADA54232
32	26	89.7	265	6	ADA36329
33	26	89.7	299	7	ADM05522
34	26	89.7	299	9	AEC88452
35	26	89.7	304	4	AAU40597
36	26	89.7	304	6	ABM37116
37	26	89.7	307	4	ABG24913
38	26	89.7	313	3	AAG44052
39	26	89.7	328	7	ADC31568
40	26	89.7	353	3	AAG44051
41	26	89.7	366	8	ABM83600
42	26	89.7	379	9	ADY65392
43	26	89.7	380	2	AAR53750
44	26	89.7	380	2	AAW48731
45	26	89.7	380	2	AAV24952

ALIGNMENTS

RESULT 1

ADU05742
ID ADU05742 standard; peptide; 6 AA.

XX AC ADU05742;

XX DT 27-JAN-2005 (first entry)

XX DE Kallikrein substrate peptide #1.

OM protein - protein search, using sw model

Run on: November 16, 2006, 22:46:28 ; Search time 176.4 Seconds
(without alignments)
23.127 Million cell updates/sec

Title: MISLMKRPQ
Perfect score: 44
Sequence: 1 mislmkrpq 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	44	100.0	9 8 ADU05743	ADU05743 Kallikrei
2	44	100.0	9 9 ADZ79590	Adz79590 Wound hea
3	44	100.0	9 9 AEB97529	Aeb97529 Kallikrei
4	44	100.0	9 9 AEC32752	Aec32752 Substrate
5	39	88.6	16 2 AAW54320	Aaw54320 Bradykini
6	39	88.6	60 4 AEG21097	Aeg21097 Novel hum
7	39	88.6	64 2 AAW54341	Aaw54341 Bradykini

8	39	88.6	64 2 AAW77418	Aaw77418 Kininogen
9	39	88.6	268 8 ADP43683	Adp43683 Human PMW
10	39	88.6	268 8 ABM83721	Abm83721 Human dia
11	39	88.6	304 6 ABP70801	Abp70801 Human ext
12	39	88.6	304 8 ABM83720	Abm83720 Human dia
13	39	88.6	322 6 ABP70799	Abp70799 Human ext
14	39	88.6	326 8 ABM83717	Abm83717 Human dia
15	39	88.6	329 6 ABU92044	Abu92044 Human pro
16	39	88.6	329 8 ABM83716	Abm83716 Human dia
17	39	88.6	357 6 ABM83715	Abm83715 Human dia
18	39	88.6	358 6 ABP70800	Abp70800 Human ext
19	39	88.6	362 9 AEB32339	Aeb32339 Human pro
20	39	88.6	362 9 AEB32341	Aeb32341 Human pro
21	39	88.6	390 6 ABU99149	Abu99149 Novel hum
22	39	88.6	390 8 ADM93863	Adm93863 Human NOV
23	39	88.6	390 8 ADT04032	Adt04032 Human pro
24	39	88.6	390 8 ADS93172	Ads93172 Novel hum
25	39	88.6	392 8 ABM83719	Abm83719 Human dia
26	39	88.6	398 6 ABU99143	Abu99143 Novel hum
27	39	88.6	398 8 ADM93851	Adm93851 Human NOV
28	39	88.6	398 8 ABM83718	Abm83718 Human dia
29	39	88.6	398 8 ADS93160	Ads93160 Novel hum
30	39	88.6	427 8 ADE76864	Ade76864 Human pro
31	39	88.6	427 8 ABM83715	Abm83715 Human dia
32	39	88.6	427 8 ABM80523	Abm80523 Tumour-as
33	39	88.6	427 8 ADQ39518	Adq39518 Human myo
34	39	88.6	427 8 ADQ39516	Adq39516 Human myo
35	39	88.6	427 8 ADS93164	Ads93164 Novel hum
36	39	88.6	579 9 AEB32342	Aeb32342 Human pro
37	39	88.6	579 9 AEB32338	Aeb32338 Human pro
38	39	88.6	612 8 ADS93142	Ads93142 Novel hum
39	39	88.6	615 6 ABU99144	Abu99144 Novel hum
40	39	88.6	615 8 ADM93853	Adm93853 Human NOV
41	39	88.6	615 8 ADS93162	Ads93162 Novel hum
42	39	88.6	616 8 ADS93154	Ads93154 Novel hum
43	39	88.6	621 8 ADS93156	Ads93156 Novel hum
44	39	88.6	621 8 ADS93184	Ads93184 Novel hum
45	39	88.6	622 8 ADS93158	Ads93158 Novel hum

ALIGNMENTS

RESULT 1
ADU05743
ID ADU05743 standard; peptide; 9 AA.
XX
AC ADU05743;
XX
DT 27-JAN-2005 (first entry)
XX
DE Kallikrein substrate peptide #2.
XX
KW antimicrobial; analgesic; anesthetic; vulnerary; kallikrein inhibitor;
KW wound dressing; oligopeptidic sequence; kallikrein.
XX
OS Unidentified.